AMENDMENTS TO THE SPECIFICATION

Please amend paragraph 0185 with the following amended paragraph:

-- A consensus pattern for casein kinase II phosphorylations site is as follows: [ST]-x(2)-[DE] SEQ ID NO:82), wherein 'x' represents any amino acid, and S or T is the phosphorylation site.--

Please amend paragraph 0189 with the following amended paragraph:

-- A consensus pattern for cAMP- and cGMP-dependent protein kinase phosphorylation sites is as follows: [RK](2)-x-[ST] SEQ ID NO:83), wherein "x" represents any amino acid, and S or T is the phosphorylation site.--

Please amend paragraph 0193 with the following amended paragraph:

--Asparagine glycosylation sites have the following concensus pattern, N-{P}-[ST]-{P} SEQ ID NO:84), wherein N represents the glycosylation site. However, it is well known that that potential N-glycosylation sites are specific to the consensus sequence Asn-Xaa-Ser/Thr. However, the presence of the consensus tripeptide is not sufficient to conclude that an asparagine residue is glycosylated, due to the fact that the folding of the protein plays an important role in the regulation of N-glycosylation. It has been shown that the presence of proline between Asn and Ser/Thr will inhibit N-glycosylation; this has been confirmed by a recent statistical analysis of glycosylation sites, which also shows that about 50% of the sites that have a proline C-terminal to Ser/Thr are not glycosylated. Additional information relating to asparagine glycosylation may be found in reference to the following publications, which are hereby incorporated by reference herein: Marshall R.D., Annu. Rev. Biochem. 41:673-702(1972); Pless D.D., Lennarz W.J., Proc. Natl. Acad. Sci. U.S.A. 74:134-138(1977); Bause E., Biochem. J. 209:331-336(1983); Gavel Y., von Heijne G., Protein Eng. 3:433-442(1990); and Miletich J.P., Broze G.J. Jr., J. Biol. Chem. 265:11397-11404(1990).--

Please amend paragraph 0196 with the following amended paragraph:

--A consensus pattern for N-myristoylation is as follows: G-{EDRKHPFYW}-x(2)-[STAGCN]-{P} SEQ ID NO:85), wherein 'x' represents any amino acid, and G is the N-myristoylation site.--

Please amend paragraph 0201 with the following amended paragraph:

--The putative concensus sequence for GPCRs comprises the conserved triplet and also spans the major part of the third transmembrane helix, and is as follows: [GSTALIVMFYWC]-[GSTANCPDE]-{EDPKRH}-x(2)-[LIVMNQGA]-x(2)-[LIVMFT]-[GSTANC]-[LIVMFYWSTAC]-[DENH]-R-[FYWCSH]-x(2)-[LIVM] SEQ ID NO:86), where "X" represents any amino acid.--

AMENDMENTS TO THE SEQUENCE LISTING

In order to comply with the Notice to Comply With Requirements For Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures, the following has been amended within the Sequence Listing:

A) Lines <140> and <141> were amended to state the U.S. Serial Number and filing date of Non-Provisional Application U.S. 09/966,422;

B) The artificial sequence definition of SEQ ID NO: 67 was changed from "Oligo 1; N=A+G+C+T; K=C+G+T" to "Synthesized Oligonucleotide" to more accurately describe the source of this artificial sequence.

C) Lines <221> thru lines <223> were added for SEQ ID NO:67 to define the "n" and "k" nucleotides as a MISC_FEATURE, and to capture the definition that was originally placed on the "Artificial Sequence" definition line.

D) The artificial sequence definition of SEQ ID NO: 68 was changed from "Oligo 2; N=A+G+C+T; V=C+A+G" to "Synthesized Oligonucleotide" to more accurately describe the source of this artificial sequence.

E) Lines <221> thru lines <223> were added for SEQ ID NO:68 to define the "n" and "k" nucleotides as a MISC_FEATURE, and to capture the definition that was originally placed on the "Artificial Sequence" definition line.

F) New sequences SEQ ID NO:82 to SEQ ID NO:86 were added to the Sequence Listing, along with the appropriate lines <221> thru <223>, to conform to 37 C.F.R. 1.821-1.825, and to address the Examiner's objection to Applicants failure to include the same.